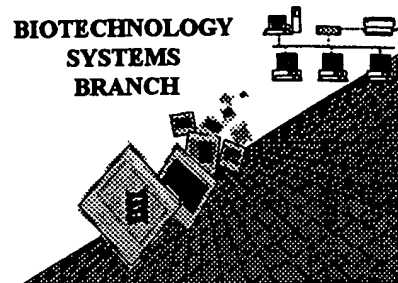*Kaustel*

# RAW SEQUENCE LISTING
# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _09/155,327_

Art Unit / Team No. : _1633_

Date Processed by STIC: _12/20/99_

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

> This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.

| 1 | <110> AMRAD Operations Pty Ltd |
|---|---|
| 2 | <120> A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2 |
| 3 | FAMILY OF APOPTOSIS-CONTROLLING GENES |
| 4 | <130> 2096584 |
| 5 | <140> US/09/155,327 |
| 6 | <141> 1999-03-29 |
| 7 | <150> PN8965 |
| 8 | <151> 1996-03-27 |

Does Not Comply
Corrected Diskette Needed

E--> 9    <160> (12) 9 (next pages)
10   <170> PatentIn Ver. 2.1

## ERRORED SEQUENCES FOLLOW

11   <210> 1
12   <211> 33
13   <212> DNA
14   <213> Mouse        "j" is invalid for use in the sequence - use n and define
15   <400> 1
E--> 16   gctctagaac tggggghgir thgthgcctt ytt                    33    (2207-2223)
                                                                       section

17   <210> 3
18   <211> 31
19   <212> DNA
20   <213> Mouse        same error
21   <400> 3
E--> 22   ggaattccca gcciccitki tcttggatcc a                      31

FYI

Please review the
**Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**

```
      cag gtt tcc gac gaa ctt ttc caa ggg ggc cct aac tgg ggc cgt ctt    28
8
      Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
                          85                  90                  95

      gtg gca ttc ttt gtc ttt ggg gct gcc ctg tgt gct gag agt gtc aac    33
6
      Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
                          100                 105                 110

      aaa gaa atg gag cct ttg gtg gga caa gtc cag gat tgg atc gtg gcc    38
4
      Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala
                          115                 120                 125

      tac ctg gag aca cgt ctg gct gac tgg atc cac agc agt ggc ggc tgg    43
2
      Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
          130                 135                 140

      gcg gac ttc aca gct cta tac ggg gac ggg gcc ctg gag gac gca cgg    48
0
      Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg
      145                 150                 155                 160

      cgt ctg cgg gag ggc aac tgg gca tga gtg agc aca gtg gtg acg ggg    52
8
      Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly Ala
                          165                 170                 175

      gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc    57
6
      Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser Lys
                          180                 185                 190

      aag tg                                                             58
1
```

*last sequence in file*

```
<400> 9
Met Pro Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp
1               5                   10                  15
```

Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
            20                  25                  30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
            35                  40                  45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
    50                  55                  60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
65                  70                  75                      80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
                85                  90                  95

Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
                100                 105                 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala
            115                 120                 125

Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
    130                 135                 140

Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg
145                 150                 155                 160

Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly
                165                 170                 175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
                180                 185                 190

Lys

PAGE:     2

VERIFICATION SUMMARY
PATENT APPLICATION US/09/155,327

DATE: 12/20/1999
TIME: 10:40:37

Input Set: I155327.RAW

| Line | ? | Error/Warning | Original Text |
|---|---|---|---|
| 9 | E | # of Seq. 12 Not Equal Actual 9 | <160>   12 |
| 16 | E | Wrong Nucleic Acid Designator | gctctagaac tggggihgir tigtigcctt ytt |
| 16 | E | Wrong Nucleic Acid Designator | gctctagaac tggggihgir tigtigcctt ytt |
| 16 | E | Wrong Nucleic Acid Designator | gctctagaac tggggihgir tigtigcctt ytt |
| 16 | E | Wrong Nucleic Acid Designator | gctctagaac tggggihgir tigtigcctt ytt |
| 22 | E | Wrong Nucleic Acid Designator | ggaattccca gcciccitki tcttggatcc a |
| 22 | E | Wrong Nucleic Acid Designator | ggaattccca gcciccitki tcttggatcc a |
| 22 | E | Wrong Nucleic Acid Designator | ggaattccca gcciccitki tcttggatcc a |